

RAW SEQUENCE LISTING  
PATENT APPLICATION US/10/052,545DATE: 02/13/2002  
TIME: 21:09:06

INPUT SET: S36758.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

## (i) APPLICANT:

(A) NAME: Jarl Wikberg  
(B) STREET: Trillvaegen 13  
(C) CITY: Umea  
(E) COUNTRY: Sweden  
(F) POSTAL CODE (ZIP): 905 92 Umea

(A) NAME: Vijay Chhajlani  
(B) STREET: Stigbergsvaegen  
(C) CITY: Uppsala  
(E) COUNTRY: Sweden  
(F) POSTAL CODE (ZIP): 752 42 Uppsala

(ii) TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor

(iii) NUMBER OF SEQUENCES: 20

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
(B) STREET: 1100 New York Ave., N.W.  
(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 20005

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 10/052,545  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/387,805  
(B) FILING DATE: 21-FEB-95

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47      (A) APPLICATION NUMBER: PCT/DK93/00273
48      (B) FILING DATE: 20-AUG-93
49
50      (vii) PRIOR APPLICATION DATA:
51      (A) APPLICATION NUMBER: DK 1046/92
52      (B) FILING DATE: 21-AUG-92
53
54      (vii) PRIOR APPLICATION DATA:
55      (A) APPLICATION NUMBER: DK 1118/92
56      (B) FILING DATE: 10-SEP-92
57
58      (vii) PRIOR APPLICATION DATA:
59      (A) APPLICATION NUMBER: DK 0528/93
60      (B) FILING DATE: 05-MAY-93
61
62      (viii) ATTORNEY/AGENT INFORMATION:
63      (A) NAME: Cimbala, Michele A.
64      (B) REGISTRATION NUMBER: 33,851
65      (C) REFERENCE/DOCKET NUMBER: 1102.0160000
66
67      (ix) TELECOMMUNICATION INFORMATION:
68      (A) TELEPHONE: (202)371-2600
69      (B) TELEFAX: (202) 371-2540
70
71      (2) INFORMATION FOR SEQ ID NO: 1:
72
73      (i) SEQUENCE CHARACTERISTICS:
74      (A) LENGTH: 1270 base pairs
75      (B) TYPE: nucleic acid
76      (C) STRANDEDNESS: double
77      (D) TOPOLOGY: linear
78
79      (ii) MOLECULE TYPE: DNA (cDNA)
80
81      (ix) FEATURE:
82      (A) NAME/KEY: CDS
83      (B) LOCATION: 169..1122
84
85      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
86      GGAGAGGGTG TGAGGGCAGA TCTGGGGGTG CCCAGATGGA AGGAGGCAGG CATGGGGGAC      60
87
88      ACCCAAGGCC CCCTGGCAGC ACCATGAACT AAGCAGGACA CCTGGAGGGG AAGAACTGTG      120
89
90      GGGACCTGGA GGCCTCCAAC GACTCCTTCC TGCTTCCTGG ACAGGACT ATG GCT GTG      177
91      Met Ala Val
92      1
93
94      CAG GGA TCC CAG AGA AGA CTT CTG GGC TCC CTC AAC TCC ACC CCC ACA      225
95      Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser Thr Pro Thr
96      5 10 15
97
98      GCC ATC CCC CAG CTG GGG CTG GCT GCC AAC CAG ACA GGA GCC CGG TGC      273
99
  
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100	Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly Ala Arg Cys	35
101	20 25 30	
102		
103	CTG GAG GTG TCC ATC TCT GAC GGG CTC TTC CTC AGC CTG GGG CTG GTG	321
104	Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu Gly Leu Val	
105	40 45 50	
106		
107	AGC TTG GTG GAG AAC GCG CTG GTG GTG GCC ACC ATC GCC AAG AAC CGG	369
108	Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala Lys Asn Arg	
109	55 60 65	
110		
111	AAC CTG CAC TCA CCC ATG TAC TGC TTC ATC TGC TGC CTG GCC TTG TCG	417
112	Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu Ala Leu Ser	
113	70 75 80	
114		
115	GAC CTG CTG GTG AGC GGG AGC AAC GTG CTG GAG ACG GCC GTC ATC CTC	465
116	Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala Val Ile Leu	
117	85 90 95	
118		
119	CTG CTG GAG GCC GGT GCA CTG GTG GCC CGG GCT GCG GTG CTG CAG CAG	513
120	Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val Leu Gln Gln	
121	100 105 110 115	
122		
123	CTG GAC AAT GTC ATT GAC GTG ATC ACC TGC AGC TCC ATG CTG TCC AGC	561
124	Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met Leu Ser Ser	
125	120 125 130	
126		
127	CTC TGC TTC CTG GGC GCC ATC GCC GTG GAC CGC TAC ATC TCC ATC TTC	609
128	Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile Ser Ile Phe	
129	135 140 145	
130		
131	TAC GCA CTG CGC TAC CAC AGC ATC GTG ACC CTG CCG CGG GCG CGG CGA	657
132	Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Arg Arg	
133	150 155 160	
134		
135	CGC GTT GCG GCC ATC TGG GTG GCC AGT GTC GTC TTC AGC ACG CTC TTC	705
136	Arg Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe	
137	165 170 175	
138		
139	ATC GCC TAC TAC GAC CAC GTG GCC GTC CTG CTG TGC CTC GTG GTC TTC	753
140	Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe	
141	180 185 190 195	
142		
143	TTC CTG GCT ATG CTG GTG CTC ATG GCC GTG CTG TAC GTC CAC ATG CTG	801
144	Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val His Met Leu	
145	200 205 210	
146		
147	GCC CGG GCC TGC CAG CAC GCC CAG GGC ATC GCC CGG CTC CAC AAG AGG	849
148	Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg	
149	215 220 225	
150		
151	CAG CGC CCG GTC CAC CAG GGC TTT GGC CTT AAA GGC GCT GTC ACC CTC	897
152	Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu	

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153	230	235	240	
154				945
155	ACC ATC CTG CTG GGC ATT TTC TTC CTC TGC TGG GGC CCC TTC TTC CTG			
156	Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro Phe Phe Leu			
157	245	250	255	
158				993
159	CAT CTC ACA CTC ATC GTC CTC TGC CCC GAG CAC CCC ACG TGC GGC TGC			
160	His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr Cys Gly Cys			
161	260	265	270	275
162				1041
163	ATC TTC AAG AAC TTC AAC CTC TTT CTC GCC CTC ATC ATC TGC AAT GCC			
164	Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile Cys Asn Ala			
165		280	285	290
166				1089
167	ATC ATC GAC CCC CTC ATC TAC GCC TTC CAC AGC CAG GAG CTC CGC AGG			
168	Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu Leu Arg Arg			
169		295	300	305
170				1139
171	ACG CTC AAG GAG GTG CTG ACA TGC TCC TGG TGAGCGCGGT GCACGCGCTT			
172	Thr Leu Lys Glu Val Leu Thr Cys Ser Trp			
173		310	315	
174				1199
175	TAAGTGTGCT GGGCAGAGGG AGGTGGTGAT ATTGTGTGGT CTGGTTCCTG TGTGACCCTG			
176				1259
177	GGCAGTTCCT TACCTCCCTG GTCCCCGTTT GTCAAAGAGG ATGGACTAAA TGATCTCTGA			
178				1270
179	AAGTGTGAA G			
180				
181				
182	(2) INFORMATION FOR SEQ ID NO: 2:			
183				
184	(i) SEQUENCE CHARACTERISTICS:			
185	(A) LENGTH: 317 amino acids			
186	(B) TYPE: amino acid			
187	(D) TOPOLOGY: linear			
188				
189	(ii) MOLECULE TYPE: polypeptide			
190				
191	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:			
192				
193	Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser			
194	1	5	10	15
195				
196	Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly			
197		20	25	30
198				
199	Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu			
200		35	40	45
201				
202	Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala			
203		50	55	60
204				
205	Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu			

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	65	70	75	80
206				
207				
208	Ala Leu Ser Asp	Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala		
209		85	90	95
210				
211	Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val			
212		100	105	110
213				
214	Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met			
215		115	120	125
216				
217	Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile			
218		130	135	140
219				
220	Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg			
221		145	150	155
222				
223	Ala Arg Arg Arg Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser			
224		165	170	175
225				
226	Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu			
227		180	185	190
228				
229	Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val			
230		195	200	205
231				
232	His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu			
233		210	215	220
234				
235	His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala			
236		225	230	235
237				
238	Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro			
239		245	250	255
240				
241	Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr			
242		260	265	270
243				
244	Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile			
245		275	280	285
246				
247	Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu			
248		290	295	300
249				
250	Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp			
251		305	310	315

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid

**SEQUENCE VERIFICATION REPORT**  
PATENT APPLICATION *US/10/052,545*DATE: 02/13/2002  
TIME: 21:09:08*INPUT SET: S36758.raw*

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Jarl Wikberg
7	Unknown or Misplaced Identifier	(B) STREET: Trillvaegen 13
8	Unknown or Misplaced Identifier	(C) CITY: Umea
9	Unknown or Misplaced Identifier	(E) COUNTRY: Sweden
10	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 905 92 Umea
12	Unknown or Misplaced Identifier	(A) NAME: Vijay Chhajlani
13	Unknown or Misplaced Identifier	(B) STREET: Stigbergsvaegen
14	Unknown or Misplaced Identifier	(C) CITY: Uppsala
15	Unknown or Misplaced Identifier	(E) COUNTRY: Sweden
16	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 752 42 Uppsala

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**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/10/052,545**

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*INPUT SET: S36758.raw*

< < THERE ARE NO ITEMS MISSING > >

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**SEQUENCE CORRECTION REPORT**  
PATENT APPLICATION *US/10/052,545*

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Line	Original Text	Corrected Text
834	(xi) SEQUENCE DESCRIPTION: SEQ ID NO 17:	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17: